

D4CO  
Page 1 of 7  
3/14/01  
#2  
OIPE

ENTERED

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/781,880  
DATE: 03/19/2001  
TIME: 13:09:42  
  
Input Set : A:\Seqlist.txt  
Output Set: N:\CRF3\03192001\I781880.raw  
  
 4 <110> APPLICANT: Glucksmann, Maria Alexandra  
 5 Silos-Santiago, Inmaculada  
 7 <120> TITLE OF INVENTION: Novel Seven-Transmembrane  
 8 Proteins/G-Protein Coupled Receptors  
 11 <130> FILE REFERENCE: 35800/208932  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/781,880  
 C--> 13 <141> CURRENT FILING DATE: 2001-02-12  
 13 <150> PRIOR APPLICATION NUMBER: 60/182,061  
 14 <151> PRIOR FILING DATE: 2000-02-11  
 16 <160> NUMBER OF SEQ ID NOS: 10  
 18 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
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 21 <211> LENGTH: 1875  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Homo sapiens  
 25 <220> FEATURE:  
 26 <221> NAME/KEY: CDS  
 27 <222> LOCATION: (323)...(1522)  
 29 <221> NAME/KEY: misc\_feature /  
 30 <222> LOCATION: (1)...(1875)  
 31 <223> OTHER INFORMATION: n = A,T,C or G  
 33 <400> SEQUENCE: 1  
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 36 agtttgcagaq gagtgagatt acatgggctt gcacctggctt ttttttgta tttaagttaa 180  
 37 agacagggtt tcaccatgtt ggcaggctg ttcttgcact cctgaccctca agtgttcccc 240  
 W--> 38 ntgcctcggtt ctccttcaaag tgtctggattt acaggcatgc accaccatcc ccagccttct 300  
 39 ctcttttttaa taatggcttt ctatgt ttc act tct ctc ata ccc tca ctc 352  
 40 Met Ser Phe Thr Ser Leu Ile Pro Ser Leu  
 41 1 5 10  
 43 tgt ttc tcc ttg act ctc cca ttc ctg ttt tgt tat ctt tct tta tgg 400  
 44 Cys Phe Ser Leu Thr Leu Pro Phe Leu Phe Cys Tyr Leu Ser Leu Trp  
 45 15 20 25  
 47 ccc ttt ctt tct gct ttt ctg ttt atc act ccc tgg cta ctt qcc ttt 448  
 48 Pro Phe Leu Ser Ala Phe Leu Phe Ile Thr Arg Trp Leu Leu Ala Phe  
 49 30 35 40  
 51 ctc tct cta ttc tct gtc tct gtc cct gtt tct tct gtt tca agt tca 496  
 52 Leu Ser Leu Phe Ser Val Ser Val Pro Val Ser Ser Val Ser Ser Ser  
 53 45 50 55  
 55 ala gtt ctc tgt atc tat ctc tct gtt tct gcc tct ccg tct gtc ttt 544  
 56 Met Val Leu Cys Leu Tyr Leu Ser Val Ser Ala Ser Pro Ser Val Phe  
 57 60 65 70  
 59 tgt ttc tct tgc atg cag ggc ccc ata ctg tgg atc atg gca aat ctg 592  
 60 Cys Phe Ser Cys Met Gln Gly Pro Ile Leu Trp Ile Met Ala Asn Leu  
 61 75 80 85 90  
 63 agc cag ccc tcc gaa ttt gtc ctc ttg ggc ttc tcc ttt ggt gag 640  
 64 Ser Gln Pro Ser Glu Phe Val Leu Leu Gly Phe Ser Ser Phe Gly Glu

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65	95	100	105	
67	ctg cag gcc ctt ctg tat ggc ccc ttc ctc atg ctt tat ctt ctc gcc			688
68	Leu Gln Ala Leu Leu Tyr Gly Pro Phe Leu Met Leu Tyr Leu Leu Ala			
69	110	115	120	
71	ttc atg gya aac acc atc atc ata gtt atg gtc ata gct gac acc cac			736
72	Phe Met Gly Asn Thr Ile Ile Ile Val Met Val Ile Ala Asp Thr His			
73	125	130	135	
75	cta cat aca ccc atg tac ttc ttc ctg ggc aat ttt tcc ctg ctg gag			784
76	Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Phe Ser Leu Leu Glu			
77	140	145	150	
79	atc ttg gta acc atg act gca gtg ccc aag atg ctc tca gac ctg ttg			832
80	Ile Leu Val Thr Met Thr Ala Val Pro Arg Met Leu Ser Asp Leu Leu			
81	155	160	165	170
83	gtc ccc cac aaa gtc att acc ttc act ggc tgc atg gtc cag ttc tac			880
84	Val Pro His Lys Val Ile Thr Phe Thr Gly Cys Met Val Gln Phe Tyr			
85	175	180	185	
87	ttc cac ttt tcc ctg agg tcc acc tcc atc ctg aca gac atg			928
88	Phe His Ser Leu Gly Ser Thr Ser Phe Leu Ile Leu Thr Asp Met			
89	190	195	200	
91	gcc ctt gat cgc ttt gtg gcc atc tgc cac cca ctg cgc tat ggc act			976
92	Ala Leu Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg Tyr Gly Thr			
93	205	210	215	
95	ctg atg agc cgg gct atg tgt gtc cag ctg gct ggg gct gcc tgg gca			1024
96	Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly Ala Ala Trp Ala			
97	220	225	230	
99	gct cct ttc cta gcc atg gta ccc act gtc ctc tcc cga gct cat ctt			1072
100	Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser Arg Ala His Leu			
101	235	240	245	250
103	gat tac tgc cat ggc ggc gtc atc aac cac ttc ttc tgt gac aat gaa			1120
104	Asp Tyr Cys His Gly Gly Val Ile Asn His Phe Phe Cys Asp Asn Glu			
105	255	260	265	
107	cct ctc ctg cag ttg tca tgc tct gac act cgc ctg ttg gaa ttc tgg			1168
108	Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Leu Glu Phe Trp			
109	270	275	280	
111	gac ttt ctg atg gcc ttg acc ttt gtc ctc agc tcc ctg gtg acc			1216
112	Asp Phe Leu Met Ala Leu Thr Phe Val Leu Ser Ser Phe Leu Val Thr			
113	285	290	295	
115	ctc atc tcc tat ggc tac ata gtg acc act gtg ctg cgg atc ccc tct			1264
116	Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Ile Arg Ile Pro Ser			
117	300	305	310	
119	gcc agc agc tgc cag aag gct ttc tcc act tgc ggg tct cac ctc aca			1312
120	Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr			
121	315	320	325	330
123	ctg gtc ttc atc ggc tac agt agt acc atc ttt ctg tat gtc agg cct			1360
124	Leu Val Phe Ile Gly Tyr Ser Ser Thr Ile Phe Leu Tyr Val Arg Pro			
125	335	340	345	
127	ggc aaa gct cac tct gtg caa gtc agg aag gtc gtg gcc ttg gtg act			1408
128	Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu Val Thr			
129	350	355	360	

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131	tca	gtt	ctc	acc	ccc	ttt	ctc	aat	ccc	ttt	atc	ctt	acc	ttc	tgc	aat		1456
132	Ser	Val	Leu	Thr	Pro	Phe	Leu	Asn	Pro	Phe	Ile	Leu	Thr	Phe	Cys	Asn		
133								365				370				375		
135	cag	aca	gtt	aaa	aca	gtg	cta	cag	ggg	cag	atg	cag	agg	ctg	aaa	ggc		1504
136	Gln	Thr	Val	Lys	Thr	Val	Leu	Gln	Gly	Gln	Met	Gln	Arg	Leu	Lys	Gly		
137								380				385				390		
139	ctt	tgc	aag	gca	caa	tga	/tqagccagg	gcccaggqqa	acctqgcctq									1552
140	Leu	Cys	Lys	Ala	Gln	*												
141	395																	
143	cctccattga	gcagtctgt	ggggaggagg	acctccagca	agtgggaaga	acactgctga												1612
144	gttttttag	ttttttccc	tctqagaaat	aactacagtg	agccctgagt	gctqcactgt												1672
145	ctqccccaaa	gcttttatqq	accaccatgg	aagagttccc	tacatcccc	ggcagcgcgt												1732
146	agaactctqa	qatqagccca	gagctttcq	taaagggaag	tgcatgtgt	ttgcatttaa												1792
147	ggaagagcag	comagaagtq	tctatgatc	aagaggtatq	cgacgcggcc	gcgtcgacgg												1852
148	aagctqgqat	acacatita	atg															1875
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157	1							5				10				15		
158	Pro	Phe	Leu	Phe	Cys	Tyr	Leu	Ser	Leu	Trp	Pro	Phe	Leu	Ser	Ala	Phe		
159								20				25				30		
160	Leu	Phe	Ile	Thr	Arg	Trp	Leu	Leu	Ala	Phe	Leu	Ser	Leu	Phe	Ser	Val		
161								35				40				45		
162	Ser	Val	Pro	Val	Ser	Ser	Val	Ser	Ser	Ser	Met	Val	Leu	Cys	Leu	Tyr		
163								50				55				60		
164	Leu	Ser	Val	Ser	Ala	Ser	Pro	Ser	Val	Phe	Cys	Phe	Ser	Cys	Met	Gln		
165								65				70				75		80
166	Gly	Pro	Ile	Leu	Trp	Ile	Met	Ala	Asn	Leu	Ser	Gln	Pro	Ser	Glu	Phe		
167								85				90				95		
168	Val	Leu	Leu	Gly	Phe	Ser	Ser	Phe	Gly	Glu	Leu	Gln	Ala	Leu	Tyr			
169								100				105				110		
170	Gly	Pro	Phe	Leu	Met	Leu	Tyr	Leu	Leu	Ala	Phe	Met	Gly	Asn	Thr	Ile		
171								115				120				125		
172	Ile	Ile	Val	Met	Val	Ile	Ala	Asp	Thr	His	Leu	His	Thr	Pro	Met	Tyr		
173								130				135				140		
174	Phe	Phe	Leu	Gly	Asn	Phe	Ser	Leu	Leu	Glu	Ile	Leu	Val	Thr	Met	Thr		
175								145				150				155		160
176	Ala	Val	Pro	Arg	Met	Leu	Ser	Asp	Leu	Leu	Val	Pro	His	Lys	Val	Ile		
177								165				170				175		
178	Thr	Phe	Thr	Gly	Cys	Met	Val	Gln	Phe	Tyr	Phe	His	Phe	Ser	Leu	Gly		
179								180				185				190		
180	Ser	Thr	Ser	Phe	Leu	Ile	Leu	Thr	Asp	Met	Ala	Leu	Asp	Arg	Phe	Val		
181								195				200				205		
182	Ala	Ile	Cys	His	Pro	Leu	Arg	Tyr	Gly	Thr	Leu	Met	Ser	Arg	Ala	Met		
183								210				215				220		
184	Cys	Val	Gln	Leu	Ala	Gly	Ala	Ala	Trp	Ala	Ala	Pro	Phe	Leu	Ala	Met		

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185	225	230	235	240
186	Val Pro Thr Val Leu Ser Arg Ala His Leu Asp Tyr Cys His Gly Gly			
187		245	250	255
188	Val Ile Asn His Phe Phe Cys Asp Asn Glu Pro Leu Leu Gln Leu Ser			
189		260	265	270
190	Cys Ser Asp Thr Arg Leu Leu Glu Phe Trp Asp Phe Leu Met Ala Leu			
191		275	280	285
192	Thr Phe Val Leu Ser Ser Phe Leu Val Thr Leu Ile Ser Tyr Gly Tyr			
193		290	295	300
194	Ile Val Thr Thr Val Leu Arg Ile Pro Ser Ala Ser Ser Cys Gin Lys			
195	305	310	315	320
196	Ala Phe Ser Thr Cys Gly Ser His Leu Thr Leu Val Phe Ile Gly Tyr			
197		325	330	335
198	Ser Ser Thr Ile Phe Leu Tyr Val Arg Pro Gly Lys Ala His Ser Val			
199		340	345	350
200	Gln Val Arg Lys Val Val Ala Leu Val Thr Ser Val Leu Thr Pro Phe			
201		355	360	365
202	Leu Asn Pro Phe Ile Leu Thr Phe Cys Asn Gln Thr Val Lys Thr Val			
203		370	375	380
204	Leu Gln Gly Gln Met Gln Arg Leu Lys Gly Leu Cys Lys Ala Gln			
205		385	390	395
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208	<211> LENGTH: 1200			
209	<212> TYPE: DNA			
210	<213> ORGANISM: Homo sapiens			
212	<400> SEQUENCE: 3			
213	atgttcitca ctctcttcata acccttactc tggtttctct tgactctccc attcttgtt			60
214	tgttatattt cttratggcc gtttctttct gcttttctgt ttatcactcg ctggctactt			120
215	gcctttctct ctctatcttc tggttctgtc cctgtttctt ctgtttaaag ttcaatgttt			180
216	ctctgtctct atctctctgt ttctgccttc cctgttctgt ttgttttc ttc ttcgtatcgac			240
217	ggccccatatac ttgttgatcat ggcaaatatcg agccaggccc ccaaatttt cttctlgggc			300
218	ttctctctct ttggtagact gcaaggccctt ctgtatqccc ctttcctcat qttttatctt			360
219	ctcgccctca tggggaaeac catcatcata gtatggtc tagctgacac ccacccatcat			420
220	acaccatcg acttcttcet gggcaatittt tcctgttgg agatctgtt aaccatgtact			480
221	cgactgtccca ggtatcttc agacactgttg gtccccccaca tggatttttcttactgtgc			540
222	ttcatgttcc agtttacttcc acatcttcc ctggggtccca cttctcttcat catctgtaca			600
223	gacatggccc ttqatgeett tggccatcc tggccacccac tgcqctatgg cactctgttg			660
224	agccgggtta tgggttccca gctggctggg gctggctgg cagctccctt ctatccat			720
225	gtaccacactt ctcttcctcc agctcatctt gataactggcc atggggcgct catcaaccac			780
226	ttcttcgttgc aataatggcc ttcctgtcag tttgtatgt ctgacactcg ctgttggaa			840
227	ttctggact ttctgtatggc ttgtacatctt gtcttcgtatcttcttctgtt gaccctcatc			900
228	tcctatggct acatagtgtac cactgtgtcgg cggatccccctt ctggccagcag ctggccaaag			960
229	gtttttccca ctgggggttcc tcacctcaca ctgtttttca tcggctttca tagtaccatc			1020
230	tttctgtatgg tccggcttgg caaaatgttcac tctgtgtcaag tccggaaatgtt ctggcccttg			1080
231	gtgactgttcac ttcttccatccc ctttttccatc ttatcttcgtt ccatcagacaa			1140
232	gttaaaaacatg tgctcatacggg gcagatgtcag aggtgttggaaag gcttttgcggcacaatgt			1200
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235	<211> LENGTH: 3630			
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237 <213> ORGANISM: Homo sapiens  
 239 <220> FEATURE:  
 240 <221> NAME/KEY: CDS  
 241 <222> LOCATION: (343)...(2334)  
 243 <400> SEQUENCE: 4  
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 245 cgcqagcgcc tqctggcgq qacqatggty accytacggg ccqggccgct qccgcttccq 120  
 246 ctgcctccqc ctccccccaga gcaacatccg aggttcggcg cagaagagcc gccgctgtqa 180  
 247 gccgtccccgt acggggccccc gcccggccg gaggagaacg ggaggggggg cgagagagcc 240  
 248 gggqagtgc ggagccggcc cggccggcage gccgctcccc agggagggag tccgcagcc 300  
 249 gaggtttctt ccaaaaaaaa aaaaaaaaaca ac atg gct qca aag 354  
 250 Met Ala Ala Lys  
 251 1  
 253 gag aaa ctg gag gca gtg tta aat gtg gcc ctg agg gtg cca agc atc 402  
 254 Glu Lys Leu Glu Ala Val Leu Asn Val Ala Leu Arg Val Pro Ser Ile  
 255 5 10 15 20  
 257 atg ctg ttg gat qtc ctg tac aga tgg gat gtc agc tcc ttt ttc cag 450  
 258 Met Leu Leu Asp Val Leu Tyr Arg Trp Asp Val Ser Ser Phe Phe Gin  
 259 25 30 35  
 261 cag atc caa aga agt agc ctt agt aat aac cct ctt ttc caq tat aag 498  
 262 Gln Ile Gln Arg Ser Ser Leu Ser Asn Asn Pro Leu Phe Glu Tyr Lys  
 263 40 45 50  
 265 tat ttg gct ctt aat atg cat tat gta ggt tat atc tta agt gtg qtg 546  
 266 Tyr Leu Ala Leu Asn Met His Tyr Val Gly Tyr Ile Leu Ser Val Val  
 267 55 60 65  
 269 ctg cta aca ttg ccc agg cag cat ctg gtt eag ctt tat ota tat ttt 594  
 270 Leu Leu Thr Leu Pro Arg Gin His Leu Val Gln Leu Tyr Leu Tyr Phe  
 271 70 75 80  
 273 ttg act gct ctg ctc ctc tat gct gga cat caa att tcc agg gac tat 642  
 274 Leu Thr Ala Leu Leu Leu Tyr Ala Gly His Gln Ile Ser Arg Asp Tyr  
 275 85 90 95 100  
 277 gtt cqg aqt gaa ctg qag ttt gcc tat gag gga cca atq tat tta qaa 690  
 278 Val Arg Ser Glu Leu Glu Phe Ala Tyr Glu Gly Pro Met Tyr Leu Glu  
 279 105 110 115  
 281 cct ctc tct atg aat cgg ttt acc aca gcc tta ata ggt cag ttg gtg 738  
 282 Pro Leu Ser Met Asn Arg Phe Thr Thr Ala Leu Ile Gly Gln Leu Val  
 283 120 125 130  
 285 gtg tgt act tta tgc tcc tgt gtc atg aaa aca aag cag att tgg ctg 786  
 286 Val Cys Thr Leu Cys Ser Cys Val Met Lys Thr Lys Gln Ile Trp Leu  
 287 135 140 145  
 289 ttt tca gct cac atg ctt cct ctg cta gca cga ctc tgc ott gtt cct 834  
 290 Phe Ser Ala His Met Leu Pro Leu Leu Ala Arg Leu Cys Leu Val Pro  
 291 150 155 160  
 293 ttg gag aca att gtt atc atc aat aaa ttt gct atg att ttt act gga 882  
 294 Leu Glu Thr Ile Val Ile Ile Asn Lys Phe Ala Met Ile Phe Thr Gly  
 295 165 170 175 180  
 297 ttg gaa gtt ctc tat ttt ctt ggg tct aat ctt ttg gta cct tat aac 930  
 298 Leu Glu Val Leu Tyr Phe Leu Gly Ser Asn Leu Leu Val Pro Tyr Asn  
 299 185 190 195

VERIFICATION SUMMARY  
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L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:34 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:35 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:38 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1